











ET	stem_loop	/tag= an	861..868	
ET		/tag= ao	864	
ET	protein_bind	/tag= ap		
ET		/bound_motif= "Oxazolidinone"	874..879	
ET	misc_binding	/tag= aq		
ET		/bound_motif= "16S rRNA"		
ET		/note= "Binds nucleotides 826-827 to form a duplex"	881..883	
ET	misc_binding	/tag= ar		
ET		/bound_motif= "16S rRNA"		
ET		/note= "Binds nucleotides 559-560 to form a duplex"	885..912	
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ET		/bound_motif= "Streptomycin"		
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ET		/bound_motif= "Streptomycin"		
ET	protein_bind	/tag= ax	915	
ET		/bound_motif= "Streptomycin"		
ET	misc_binding	/tag= ay	916..918	
ET		/bound_motif= "16S rRNA"		
ET		/note= "Binds nucleotides 19-17 to form a duplex"	921..933	
ET	misc_binding	/tag= az		
ET		/bound_motif= "16S rRNA"		
ET		/note= "Binds nucleotides 1396-1484 to form a duplex"	926	
ET	protein_bind	/tag= ba		
ET		/bound_motif= "Kasugamycin, Edeline"	938..943	
ET	misc_binding	/tag= bb		
ET		/bound_motif= "16S rRNA"		
ET		/note= "Binds nucleotides 1345-1340 to form a duplex"	946..955	
ET	misc_binding	/tag= bc		
ET		/bound_motif= "16S rRNA"		
ET		/note= "Binds nucleotides 1235-1225 to form a duplex"	960..975	
ET	stem_loop	/tag= bd	984..990	
ET	misc_binding	/tag= be		
ET		/bound_motif= "16S rRNA"		
ET		/note= "Binds nucleotides 1221-1215 to form a duplex"	997..1003	
ET	misc_binding	/tag= bf		
ET		/bound_motif= "16S rRNA"		
ET		/note= "Binds nucleotides 1044-1037 to form a duplex"	1007..1022	
ET	stem_loop	/tag= bg	1025..1036	
ET	stem_loop	/tag= bh		
ET		/tag= bi	1037..1044	
ET	misc_binding	/tag= bi		

Query Match	86.6%	Score 1259.6	DB 22	Length 1512
Best Local Similarity	70.8%	Pred. No. 0		
Matches 1050	Conservative 256	Mismatches 61	Indels 1	Gaps 12

  

QY	1	ggcaggccaaacatgcga-tcgacggcgacggaaataagcttgcacattgcgcgcgc	59

[illegible]

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QY 114) ggtgagatgaatgaatcatcatgagcccttactagagtaggagatcatgctgatacat 1199
Dh 118. ggtgagaggaagagatgagatgagatgagatgagatgagatgagatgagatgagatg 1240
QY 120) ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatg 1259
Dh 124. ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatg 1300
QY 126) ttcgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 1319
Dh 130) ttcgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 1360
QY 132) ggtgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 1367
Dh 136) ggtgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 1408

RESULT 5
AAC62270
ID AAC62270 standard, DNA, 1542 BP.
XX
AC AAC62270;
XX
DT 19-APR-2001 (first entry)
XX
DE Escherichia coli reference 16S rDNA sequence
XX
KM 16S rDNA: dechlorinating activity; chlorinated compound; vinyl chloride;
KM carboxyethylchloride; tetrachloroethane; chloroform; dichloromethane;
KM trichloroethane; dichloroethylene; chlorinating bacteria; ss
XX
OS Escherichia coli.
XX
PN W020006444-A2
XX
PD 26-0CT-2000
XX
PF 13-APR-2000; 2000W0-0509883
XX
PR 15-APR-1999; 990S-0129511.
XX
PA (DUO) DU PONT DE NEMOURS & CO E. I.
XX
PI Hendrickson ER, Ebersole RC.
XX
DR WPI: 2001-024581/03
XX
PT New 16S rDNA profile derived from Dehalococcoides ethenogenes and
PT indicative of a dechlorinating bacterial strain.
PS Dislosure, Page 55; 53pp; English.
XX
CC The present sequence represents a reference 16S rDNA sequence. The
CC specification describes 16S rDNA sequences derived from various strains
CC of Dehalococcoides ethenogenes. These 16S rDNA profile is linked to
CC dechlorinating activity. Bacterial strain completing the 16S rDNA
CC sequence of the invention are useful for the dechlorination of
CC chlorinated compounds such as carboxyethylchloride, tetrachloroethane,
CC chloroform, dichloromethane, trichloroethylene, dichloroethylene, vinyl
CC chloride, and chloroformatics. The 16S rDNA sequence is also useful for
CC identification of new chlorinating bacteria, as well as sub-typing
CC strains of Dehalococcoides ethenogenes.
XX
SQ Sequence 1542 BP, 380 A, 352 C, 480 G, 314 T, 0 other.

Query Match 86.6%; Score 1259.6; DB 22; Length 1542;
Best Local Similarity 95.5%; Fred No. 0.
Matches 1306; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
QY 1 ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatgagat
Dh 118 ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatgagat

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Dh 101 ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatgagat
QY 120 ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatgagat
Dh 161 ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatgagat
QY 180 ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatgagat
Dh 221 ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatgagat
QY 240 ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatgagat
Dh 281 ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatgagat
QY 300 ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatgagat
Dh 341 ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatgagat
QY 360 ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatgagat
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QY 420 ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatgagat
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QY 480 ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatgagat
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Dh 1121 ggtgagatgaatgaatgagatgagatgagatgagatgagatgagatgagatgagatgagat

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QY	42)	ggttaataacctcaacgctcaatcaacttcaaccccaagaagaagacacggttaactccggatga	4750
Db	46	agtttaataacgtttgttcattatgactttaccccggaatgaatgggttttttttttttttttt	5200
QY	48)	gcacgcgcgcgtlaataacggaggggtttctatgggtttatcttgggtttatggtttg	5750
Db	52)	gcacgcgcgcgttaataacggaggggtttctatgggtttatcttgggtttatggtttg	6300
QY	54)	gcacgcgcgcgttaataacggaggggtttctatgggtttatcttgggtttatggtttg	6850
Db	58)	gcacgcgcgcgttaataacggaggggtttctatgggtttatcttgggtttatggtttg	7400
QY	60)	aactgcgcgcgttaacgctcttcttcttcttcttcttcttcttcttcttcttcttcttctt	7950
Db	64)	tactgcgcgcgttaacgctcttcttcttcttcttcttcttcttcttcttcttcttcttctt	8500
QY	66)	tagaactcttgcgaagaataacccggttcggaagagcgccccctccgacaaagacgtacacg	9050
Db	70)	tagaactcttgcgaagaataacccggttcggaagagcgccccctccgacaaagacgtacacg	9600
QY	72)	gtgcgaagacgttcgggaacaaacacgaatctatcttcttcttcttcttcttcttcttctt	10150
Db	76)	gtgcgaagacgttcgggaacaaacacgaatctatcttcttcttcttcttcttcttcttctt	10700
QY	78)	gtgcgaagacgttcgggaacaaacacgaatctatcttcttcttcttcttcttcttcttctt	11250
Db	82)	gtgcgaagacgttcgggaacaaacacgaatctatcttcttcttcttcttcttcttcttctt	11800
QY	84)	gctcgggagagtcagcgccggaaggttaaaacttaaatgaattgaattgaattgaattgaatt	12350
Db	88)	gctcgggagagtcagcgccggaaggttaaaacttaaatgaattgaattgaattgaattgaatt	12900
QY	90)	ggttcggaacgttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	13450
Db	94)	ggttcggaacgttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	14000
QY	96)	gagaactcttcgaagatgagattgtgtccttcgggaactctgaagaacgggttcggttcggt	14550
Db	100)	cgggaactcttcgaagatgagattgtgtccttcgggaactctgaagaacgggttcggttcggt	15100
QY	102)	gttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	15650
Db	106)	gttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	16200
QY	108)	tttgttcggaacgttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	16750
Db	112)	tttgttcggaacgttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	17300
QY	114)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	17850
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QY	120)	gttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	18950
Db	124)	gttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	19500
QY	126)	tcgcgaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	20050
Db	130)	tcgcgaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	20600
QY	128)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	21150
Db	132)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	21700
QY	134)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	22250
Db	138)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	22800
QY	136)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	23350
Db	140)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	23900
QY	138)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	24450
Db	142)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	25000
QY	140)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	25550
Db	144)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	26100
QY	142)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	26650
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QY	140)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	27750
Db	144)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	28300
QY	142)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	28850
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QY	140)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	29950
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QY	140)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	32150
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QY	142)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	33250
Db	146)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	33800
QY	140)	ggttcggaactcttcggtttaatctgcatacgcgaagacgttcggtttaatctgcatacgcga	34350
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Db</			

[illegible]









	Matches	1305: Conservative	0: Mismatches	61: Indels	2: Gaps
QY	1	ggcgggcttaacaaatgcaatcgaagggaggggaaggaagatgctgctacttgcgcggg	59		
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QY	60	agcgagcgagcgaggtgagtaattgtctggaaacaaacgcctgagtggtgaggtatataatgta	119		
Db	81	agtgagcgagcgaggtgagtaattgtctggaaacaaacgcctgaggtgaggtatataatgta	40		
QY	120	aacagctgtgctaatccgcgcataacggtcccaaaccaaaagaggggaaccttcgagcctctta	175		
Db	141	aacagctgtgctaatccgcgcataacggtcccaaaccaaaagaggggaaccttcgagcctctta	200		
QY	180	ccctcaagatggcccgcaatgagatagatagatagatgggtgaggttaaggttccacttggagac	249		
Db	201	ccctcaagatgcttgcgcgaatgagatagatagatagatgggtgaggttccacttggagac	260		
QY	240	gacccctagctgtgtctgagagagatgacagacacacatgaaacttggacacgtctccagact	299		
Db	261	gacccctagctgtgtctgagagagatgacacacacacatgaaacttggacacgtctccagact	320		
QY	300	ccttcgcgggagggcagcagttggggatcttgacaaatggggccaaagccgctgagcgacatgg	359		
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QY	360	cgcgtctgataagaagaagccctcgtgtctgataaagtaacttaagcgggttagagaaatgcttga	419		
Db	381	cgcgtctgataagaagaagccctcgtgtctgataaagtaacttaagcgggttagagaaatgcttga	440		
QY	420	ggtttatataatctcgcgcgattatagctgtccgcgcggtatggaggggtttatctgtgtgtgt	479		
Db	441	ggtttatataatctcgcgcgattatagctgtccgcgcggtatggaggggtttatctgtgtgtgt	500		
QY	480	ggagcgcgcggttaatacggaggtgttcgaagcgtttatcagttatattggtgtttatagtcgac	519		
Db	501	ggagcgcgcggttaatacggaggtgtgttcgaagcgtttatcagttatattggtgtttatagtcgac	560		
QY	540	gcaaggcggtctgtcaagttcgatgttgaaatcccccgtgtcccaacgtgtgtatagatggtgtgt	599		
Db	561	gcaaggcggtctgtgtcaagttcgatgttgaaatcccccgtgtcccaacgtgtgtatagatggtgtgt	620		
QY	600	aacgtggagcgttaatacgtctcttgtaagggcggttaaatccagctctttagcgggttaaaatggt	639		
Db	621	aacgtggagcgtctgtgtcgtctctctgt	660		
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QY	780	gtccacttgaggggtgtgacctttagagcgttggcttcggagacataagcgtttaatcttgcac	839		
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QY	840	gctcgtgggtgagtaaggcgccgaaggtttaaaactcaattgaattgaacgtgggtgcgggaataac	899		
Db	861	gctcgtgggtgagtaaggcgccgaaggtttaaaactcaattgaattgaacgtgggtgcgggaataac	920		
QY	900	ggttgagagatgtgtttaattcagttacgaacggagaagaccttaactcactttgaacatcaca	959		
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QY	960	gagaacattccagagatggatttggtgccttcgggaacctctagagaaagtgtgtgacatgct	1019		
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QY	1020	gtcttcagctgtgtgtgtgacatcttggtttaattcccgacacaaatggacacctcttctc	1079		
Db	1041	gtcttcagctgtgtgtgtgacatcttggtttaattcccgacacaaatggacacctcttctc	1100		

[illegible]





